SEQUENCE LISTING

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Joyal, John L
Gosselin, Michael

<120> THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR TREATING AN AMYLOIDOGENIC DISEASE

<130> PPI-105

<140> 10/996357
<141> 2001-11-27

<150> 60/253,302
<151> 2000-11-27

<150> 60/250,198
<151> 2000-11-29

<150> 60/257,186
<151> 2000-12-20

<160> 46

<170> PatentIn Ver. 2.0

<210> 1
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1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
35 40

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<400> 3

Leu Val Phe Phe Ala
1 5

<210> 4
<211> 8
<212> PRT
<213> Homo sapiens

<400> 4
Ala Gly Ala Ala Ala Ala Gly Ala
1 5

<210> 5
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1 5

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<210> 8
<211> 22
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<213> Homo sapiens

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro
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<210> 9
<211> 15

<212> PRT
<213> Homo sapiens

<400> 9
Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala
1 5 10 15

<210> 10
<211> 232
<212> PRT
<213> Homo sapiens

<400> 10
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

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aagcttgtat tcttcgcaga agacgtcgga tcgaacaaag gtgccgagcc caaatcttgt 120
gacaaaactc acacatgccc accgtgccca gcacctgaac tcctgggggg accgtcagtc 180
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ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac 360
cgggtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag 420
tgcaaggtct ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa 480
gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggatga gctgaccaag 540
aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 600
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc 660
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg 720
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 780
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<220>
<223> Description of Artificial Sequence:alpha-beta(16-30)Fc

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
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Ala Val Phe Val Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn
             20   25   30

Lys Gly Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
         35   40   45

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
     50   55   60

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 65   70   75   80

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
                 85   90   95

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
            100   105   110

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
        115   120   125

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    130   135   140

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
145   150   155   160

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Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
                165                 170                 175

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            180                 185                 190

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        195                 200                 205

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    210                 215                 220

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
225                 230                 235                 240

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                245                 250                 255

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
            260                 265


<210> 13
<211> 247
<212> PRT
<213> Homo sapiens

<400> 13
Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Glu
  1               5                  10                  15

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
             20                  25                  30

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
         35                  40                  45

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
     50                  55                  60

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 65                  70                  75                  80

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
                85                  90                  95


Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            100                 105                 110

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
        115                 120                 125

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    130                 135                 140

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
145                 150                 155                 160

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
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                165                 170                 175

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            180                 185                 190

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
        195                 200                 205

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
    210                 215                 220

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
225                 230                 235                 240

Leu Ser Leu Ser Pro Gly Lys
                245
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<210> 14
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<400> 15
gatccactag ttcttctgaa g 21

<210> 16
<211> 9
<212> PRT
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<220>
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<400> 16
Ala Arg Phe Arg Arg Thr Ser Ala Ser
 1   5

<210> 17
<211> 33
<212> DNA
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<400> 17
ttagcgcgct tcagaagaga cgcagaattc cgt 33

<210> 18
<211> 42
<212> DNA
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<400> 18
ttagcgcgct tcagaagagg cggtggtgac gcagaattcc gt 42

<210> 19
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<400> 19
ctgcgtctta aggcagtact gaggcctatg cttcacgtg 39

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<212> DNA
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<220>
<223> Synthetic construct

<400> 21
gaacataaga agcgtcttct gcagcctagg ttgtttccac 40

<210> 22
<211> 39
<212> DNA
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<400> 22
ggatccaaca aaggtgccat aataggcctt atggtaggt 39

<210> 23

<211> 33
<212> DNA
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<220>
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<400> 23
ccggaatacc atccacctca tcactgatca ggt 33

<210> 24
<211> 39
<212> DNA
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<400> 24
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<210> 25
<211> 126
<212> DNA
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 1 5 10 15

ctt gta ttc ttc gca gaa gac gtc gga tcc aac aaa ggt gcc ata ata 96
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
 20 25 30

ggc ctt atg gta ggt gga gta gtg ata gca 126
Gly Leu Met Val Gly Gly Val Val Ile Ala
 35 40

<210> 26
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 26
Leu Val Phe Phe Ala
 1 5

<210> 27
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
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<400> 27
Leu Val Phe Phe Leu
 1   5

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 28
Gly Gly Gly Leu Val Phe Phe Ala
 1   5

<210> 29
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<212> DNA
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<400> 29
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<210> 30
<211> 39
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<400> 30
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<210> 31
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<400> 31
Leu Val Phe Phe Ala
 1   5

<210> 32
<211> 30

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<400> 32
cgcgcttcag aagacttgta ttcttcgcaa 30

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ctagttgcga agaatacaag tcttctgaag 30

<210> 34
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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<400> 34
Gly Gly Gly Leu Val Phe Phe Leu
1 5

<210> 35
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<210> 36
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<400> 36
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<210> 37
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<212> PRT
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<220>

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<400> 37
Leu Val Phe Phe Leu
1 5

<210> 38
<211> 30
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cgcgcttcag aagacttgta ttcttcctta 30

<210> 39
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ctagtaagga agaatacaag tcttctgaag 30

<210> 40
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tggactagta cctttgttgg atccgac 27

<210> 41
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<220>
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<400> 41
ttagcgcgct tcagaagata cgaagtgcac caccaa 36

<210> 42
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<400> 42
ttagcgcgct tcagaagagg cggtggttac gaagtgcacc accaa 45

<210> 43
<211> 27
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<220>
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<400> 43
tggactagtt ccgacgtctt ctgcgaa 27

<210> 44
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<400> 44
ttagcgcgct tcagaagaaa gcttgtattc ttcgca 36

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<211> 45
<212> DNA
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<210> 46
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